In the Specification:

Please replace the paragraph at page 1, line 18 through page 2, line 2, with the following amended paragraph:

Iron deficiency is one of the most common human nutritional disorders in the world today (see the website at ~~http://www.~~who.int/nut/ida.htm; Yip, R. (1994) *J. Nutr.* 124: 1479S-1490S). Indeed, iron is an essential nutrient for virtually all organisms because it plays a critical role in important biochemical processes such as respiration and photosynthesis. Although abundant in nature, iron is often available in limited amounts because the oxidized form, Fe(III), is extremely insoluble at neutral or basic pH. This fact is of particular importance to agriculture because approximately one-third of the world's soils are classified as iron-deficient (Yi, Y. *et al.* (1994) *Plant Physiol.* 104: 815-820). Many "iron-efficient" plant varieties have iron uptake strategies (designated strategy I or strategy II) that are directed at solubilizing iron (Römheld, V. (1987) *Physiol. Plant.* 70: 231-234). Strategy II plants, which include all of the grasses, release Fe(III) compounds called "phytosiderophores" into the surrounding soil that bind iron and are then taken up into the roots. Most other iron-efficient plants use strategy I and respond to iron deprivation by inducing the activity of membrane-bound Fe(III) chelate reductases that reduce Fe(III) to the more soluble Fe(II) form. The Fe(II) product is then taken up into the roots by an Fe(II) specific transport system that is also induced by iron-limiting growth conditions. Furthermore, the roots or strategy I plants release more protons when iron-deficient, lowering the rhizosphere pH and thereby increasing the solubility of Fe(III). Thus, it would be desirable to take advantage of this understanding of iron-uptake strategies to produce plants which have increased iron-uptake capabilities.

Please replace the paragraph at page 55, lines 24-35, with the following amended paragraph:

Arabidopsis lines and growth conditions: The *Arabidopsis* (*Arabidopsis thaliana*) mutants *frd3-1*, *frd3-2* and the corresponding Columbia *gl-1* wild type have been described previously (Yi (1995) *Iron uptake in Arabidopsis thaliana*, Ph.D., Dartmouth College, Hanover, NH). *man1* was obtained from the *Arabidopsis* Biological Resource Center (see the website at ~~http://www.~~biosci.ohio-state.edu/~plantbio/Facilities/abrc/abrchome.htm). Unless otherwise specified, plants were grown under sterile conditions as described previously (Yi and Guerinot (1996) Plant J. 10:835-844). Briefly, seeds were sown on Petri plates containing Gamborg's B5 media (Sigma) and grown until the 4 to 6 true leaf stage and then transferred to

plates with or without 50 μM Fe(III) EDTA for iron-sufficient or deficient conditions, respectively, for three days prior to analysis. Both Fe(III) chelate reductase assays and the pH plates were also described previously (Yi and Guerinot (1996)).

Please replace the paragraph at page 57, lines 19-34, with the following amended paragraph:

frd3 Mapping and Complementation: CAPS, SSLP (simple sequence length polymorphism), and RFLP (restriction fragment length polymorphism) markers, publicly available on the *Arabidopsis* Information Resource (TAIR) web page at arabidopsis.org (~~http://www.arabidopsis.org/home.html~~), were used where possible to obtain a rough map position of *frd3*. AtMLP3, F6, and F7, are SSLP markers constructed around simple sequence repeats in the corresponding BAC sequence. F9 is an RFLP marker identified experimentally. The polymorphism covered by F11 is from the Cereon *Arabidopsis* Polymorphism Collection (available on the TAIR web site) and was scored by sequencing PCR products of that region. The complementing clone was constructed by digesting BAC T8G24 and ligating the total digest into the binary vector pCambia2300, available on the internet at the website of cambia.org.au (~~http://www.cambia.org.au/~~) according to standard molecular biology procedures (Ausubel *et al.* (2001)). The resulting clones were screened by PCR for the construct of interest. The complementing clone was introduced into the *frd3-1* mutant by *Agrobacterium*-mediated transformation (Clough and Bent (1998) Plant J. 16:735-743). 5'RACE was performed according to the instruction manual for the 5'RACE System for Rapid Amplification of cDNA Ends, Version 2.0 (Life Technologies).

Please replace the paragraph at page 58, lines 1-9, with the following amended paragraph:

DNA and Protein Sequence Analysis: DNA sequencing was performed at the Dartmouth Molecular Biology Core Facility on an ABI Prism 3100 Automated DNA Sequencer. Sequence was analyzed with the GCG (Genetics Computer Group) software package and by BLAST available on the internet at the website of ncbi.nlm.nih.gov (~~http://www.ncbi.nlm.nih.gov/BLAST/~~). Multiple sequence alignments were performed using the BCM Search Launcher available on the internet at the website of dot.imgen.bcm.tmc.edu:9331/multi-align/multi-align (~~http://dot.imgen.bcm.tmc.edu:9331/multi-align/multi-align.html~~). These alignments were transformed into dendograms using MEGA version 2.1 available on the internet at the website of megasoftware.net

~~(http://www.megasoftware.net/)~~ or colored using BoxShade available on the internet at the website of embnet.org ~~(http://www.ch.embnet.org/software/BOX_form.html)~~.